





















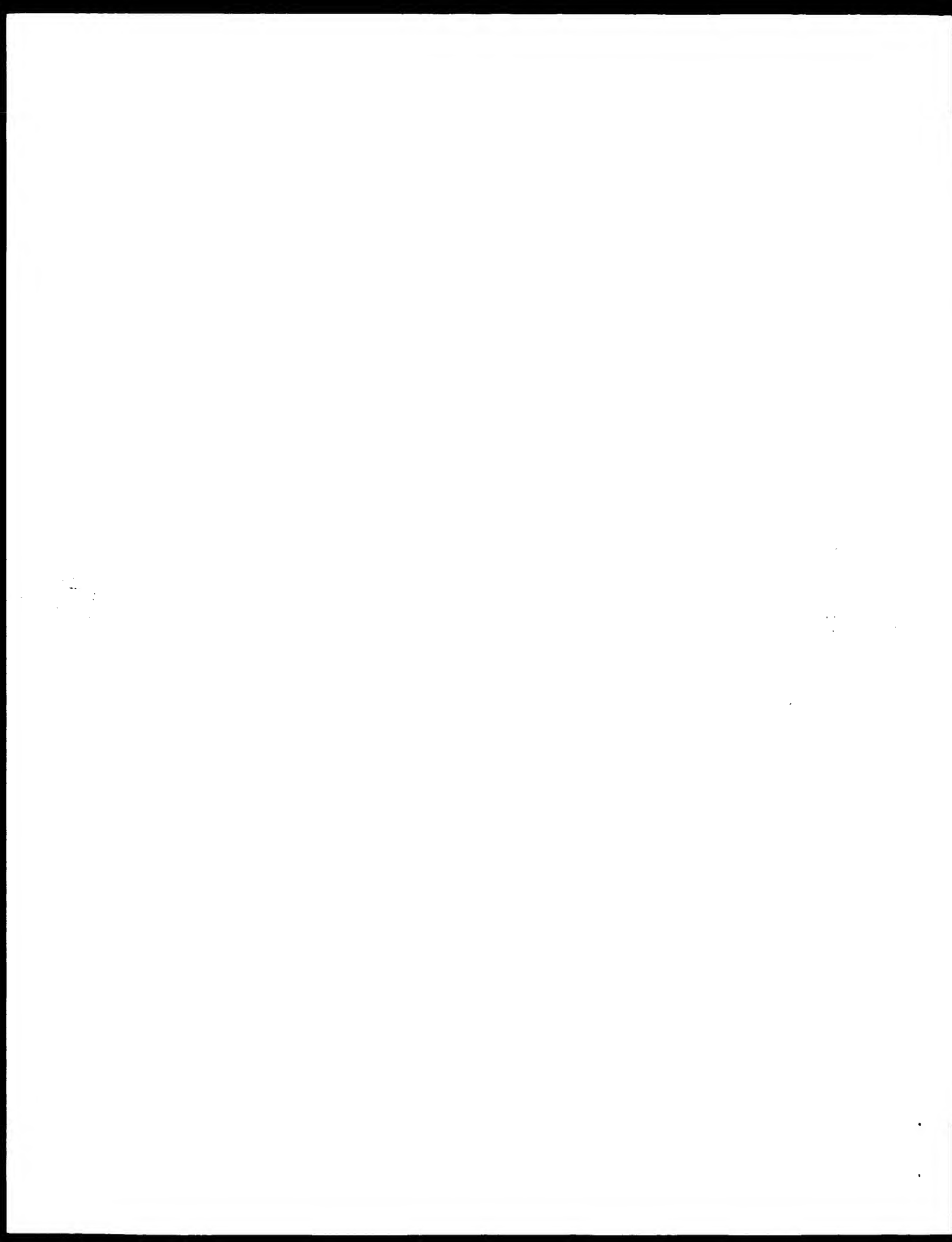




[illegible]

[illegible]

Search completed: January 10, 2003, 15:40:32  
Job name: 114.secs





















; GENERAL INFORMATION:

APPLICANT Wang, Tongming  
APPLICANT Fan, Jiquan  
APPLICANT Carlos, Miguel E.  
APPLICANT Banquet, Chantalyna S  
APPLICANT Hosken, Nancy  
APPLICANT Fanger, Gary R.  
APPLICANT Li, Samuel X.  
APPLICANT Wang, Aijiao  
APPLICANT Skeiky, Yasir A.W.  
APPLICANT Henderson, Robert A  
APPLICANT McNeill, Patricia L  
APPLICANT Fanger, Neil  
  
TITLE OF INVENTION COMPOSITIONS FOR  
TITLE OF INVENTION AND DESIGN  
FILE REFERENCE ZL97-01-5714  
CURRENT APPLICATION NUMBER US/  
CURRENT FILING DATE 2030-02-1  
NUMBER OF SEQ ID NOS 419  
SOFTWARE FASTSEQ for Windows V  
SEQ ID NO 64  
LENGTH 244  
TYPE DNA  
ORGANISM Homo sapiens

US-09 735 786 468







Percent Similarity:	39.34%	Conservative:	41
Best Local Similarity:	21.05%	Mismatches:	79
Query Match:	5.40%	Indels:	60
DB:	4	Gaps:	18
US-99	829-592+2 (1-200) X 95.9% 4.2% 45% A 1 (1-444)		
QY	9	ArgAlaSerSerLeuGlyGlySerGlyValGlyGluValIle	city 23
DB	638	CARGGGTGTGGTCTGTGGACTTGGTTCCTGCTAAATGCTGCTCTTCTCAAGTGG	100%
QY	24	LysGlyHisProHisAlaArgValValGlyValArgLysAlaGlnIleProGluIleArgGlu	43
DB	718	CTAGGACAAAGCAATCAACTACATACACACACACACACACACACACACACACAC	100%
QY	44	GluGluSerValLysProLysMetValAlaGluSerIleHisLeuAsnLeuGlnProGluGlu	63
DB	775	---CTGTGCAITATCTGCAGAAATCATGAAATATGCAATATCTCTTAAGGCATACGCTG	84
QY	64	ArgGluAlaPheCysArgLeuGluGluAsnGluGlnIleGluGlnPheLeuSerMetAsp	83
DB	842	GAAAGAGCAATGCAAAAATATGATGGAAATATAGAAATAGAAATAGAAATAGAA	87%
QY	84	SerCysLeuArgLeuSerAspLysPtyrLeuIleAlaMetValLeuAlaPtyrPheLysArg	103
DB	877	---CTGGAAGTCATCTGCAAG---GAGGCTATGTCATATATCTTCAATAGCT	92
QY	104	AlaAlaCysLeuPtyrThr	109
DB	922	TGACATCTCTCTCTCTGCAAGATCTCTGGGCTCTTATCTTGGCTCTCTCTCTCTCT	98
QY	116	SerGluPtyrThrMetAspPheValAlaGluPtyr	122
DB	982	ATCAAGAAATATATCTGCAAAAATATATATATATATATATATATATATATATAT	104
QY	123	LeuAlaAsnAspMetGluGluAspGluAspPtyrLysPtyrGlnIlePheProGluPala	142
DB	1042	ATCGGAGTCACTCGGAA---	103
QY	143	LeuGlyAspSerTrpArgGluLeuPheProGluPheLeuArgLeuArgAspPheTrp	162
DB	1072	GTA CAACATGCTATGCACTCTCTTGAGCAATATAAACAAAATACAGCATCTTTA	1129
QY	163	AlaGlyMetAsnPtyrArgAlaValValSerArgArgCysAspGluValMetSerLys	182
DB	1126	CAAGAGCAAGAAATATAGACATTTGCAATATATATTAAGCAATATATATATATAT	100%

QY 183 AspGthrHisTrpAlaTrp LeuAlaAspArqProMetHisSerHisSerGlyAlaMetAla 209  
::: ::: :::: ::::

D6 1146 AATCGAACAGCCTTTC - TGGACAGACGGA 1150; 1218  
::: ::: ::::

QY 202 gGCTyTLeuArgAcnGluActe 209  
||||| |:::

D6 1219 CAATTATTGAGAAAGAAAAA 1240

RESULT 1  
US 09 425-453A - 4  
: Sequence 3, Application US/09425453A  
: Patent NO. 6468793  
: GENERAL INFORMATION:  
: APPLICANT: Icm, John L.  
: TITLE OF INVENTION: CTR Genes and Proteins for Cystic Fibrosis Gene Therapies  
: FILE REFERENCE: FSI-94XC1  
: CURRENT APPLICATION NUMBER: US/09/425,453A  
: CURRENT FILING DATE: 1999-10-22  
: PRIOR APPLICATION NUMBER: 66/105,444  
: PRIOR FILING DATE: 1998-10-24  
: NUMBER OF SEQ ID NOS: 20  
: SUBSTANCE: Polypeptide, Nucleic Acid

```

; SEQ ID NO 1
;
; LENGTH: 444
;
; TYPE: DNA
;
; ORGANISM: Homo sapiens

```

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; FEATURE:
; NAME/KEY: qmc
; LOCATION: (1) .. (4443)
US-09-425 45A-

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Alignment Scores:

Frequency Score:			
Prod. No.	6.12	Locality	4443
Score	86.50	Chertus	48
Percent Similarity	39.04%	Observations	41
Best Local Similarity	21.05%	Mammals	79
Query Match	5.30%	Reptiles	60
DB	4	Grass	10

US-09-889 592 z (1-300) x US-0:-42' 15A (1-444)

[illegible]

## RESULTS

REF: SOL 14  
US-09-125-1E2A-5

US-09-42194-A  
; Sequence 5, Application US/142543A

; Patent No. 6,468,793

; PATIENT NO. 9400733  
; GENERAL INFORMATION

APPLICANT: Team, John L.

**TITLE OF INVENTION:** CFTR Genes and Proteins for Cystic Fibrosis Gene Therapy

FILE OF INVENTION: FIK 6155 AND 6156  
FILE REFERENCE: FSU-69X1

FILE REFERENCE: FSD-49A-1	CURRENT APPLICATION NUMBER	US/ /42/ 454A
---------------------------	----------------------------	---------------

; CURRENT APPLICATION NUMBER: US/99-10-2  
 ; CURRENT FILING DATE: 1999-10-2



















FT /\*tag a  
 XX /product: "IS26"

UN EP1026244-A1.

XX 09-AUG 2000.

XX 03-FEB-1999; 99EP-0102172.

XX 03-FEB-1999; 99EP-0102172.

XX (EMBL) EMBL EURO LAB MOLEKULARBIOLOGIE.

XX WPI: 2000-516092/47.

XX P-PSDB; AAB07752.

XX Polynucleotide encoding a protein for inducing oocyte maturation and/or  
 PT promoting cell division, proliferation and differentiation useful for  
 PT treating cancer and disorders associated with fertility.

XX Claim 1; Page 6; 17pp; English.

XX The present sequence encodes a protein which induces oocyte maturation  
 CC and promotes cell division, proliferation and differentiation. The  
 CC protein is a cell differentiation promoter. Phadaxeckal compositions  
 CC comprising the protein or polynucleotide are useful for treating cancer  
 CC or other pathological situations with uncontrolled cell growth by  
 CC promoting cell division, differentiation and proliferation and is also  
 CC useful for fertility treatments by promoting oocyte maturation. The  
 CC polynucleotides are useful as diagnostic markers for cell proliferation  
 CC and differentiation and for hybridisation experiments to determine the  
 CC amount of homologous nucleic acid sequences. They are also useful as a  
 CC target for identification of drugs that block cell cycle progression,  
 CC proliferation and differentiation.

XX Sequence 1575 BP; 406 A; 368 C; 374 G; 427 T; 0 other:

XX Alignment Scores:

Prod. No.: 2-980 168 Length: 1575  
 Score: 1632.00 Matches: 400  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 21 Gaps:

US-09-889-592-2 (1-300) x AAA59327 (1-1575)

QY 1 MetArgHisMetGlnSerValThrArgAlaSerSerIleCysGlyGlyCylValLysGln 20  
 DB 214 ATGAGGACATGACAGACTATACCGAGGCGACTGCTATTGTTGGAGGAGGATGAGGAG 274  
 QY 21 ValIleCylGlyCysGlyHisProHisAlaArgValValGlyAlaArgGlyAlaGlnIlePro 40  
 DB 274 GTATTGCAAGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 333  
 QY 41 GluArgGlnIleLeuSerValLysProLysMetValArgAsnThrIleLeuAsnLeuGln 60  
 DB 334 GAGACAGACAGAGTGTGACATGAACTGAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 394  
 QY 61 ProGlnGluArgGlnAlaPheTyArgLeuLeuGluAlaAsnGlnIleIleGlnIlePheLeu 80  
 DB 394 GCGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 453  
 QY 81 SerMetAspSerCysLeuArgIleSerAspGlySerLeuIleGlnMetValLeuAlaIle 100  
 DB 454 TCTATGAGCTCTGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 513  
 QY 101 PheLysArgAlaAlaGlyLeuTyThrSerGlnTyThrThrMetAsnPhePheValAla 120  
 DB 514 TTAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 574  
 QY 121 LeuTyLeuAlaAsnAspMetGluGluAspGluGluAspTyLeuIlePhePro 140  
 DB 574 CTTATGCTGAGTAAATGAGTAAATGAGTAAATGAGTAAATGAGTAAATGAGTAAATGAGTAA 634  
 QY 141 TrpAlaLeuGlyAspSerTrpArgGlnLeuPheProGlnIlePheLeuAlaAspAsp 160  
 DB 634 TGGCAGTACGAGACGCTGCTGAGCTTTTCTGAAATTTTCTGCTGCTGCTGCTGCTGCTGCT 694  
 QY 161 PheTrpAlaLysMetAsnTyArgAlaValValSerArgAsnArgGlyGlyValMet 180  
 DB 694 TCTGGGTAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 754  
 QY 181 SerLysAspProThrHisTrpAlaIlePheArgAspArgProMetHisHisSerGlyAla 200  
 DB 754 TCGAAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 814  
 QY 201 MetArgGlyTyLeuArgAsnGlnAspAspPhePheProGlnIlePheProGlnIlePro 220  
 DB 814 ATGCTGCTTACCTTACCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 874  
 QY 221 AlaGlnGlySerThrLeuGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 240  
 DB 874 GTCAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 934  
 QY 241 AsnSerSerProGlnIleGlnIlePheHisTyrThrAsnArgGlnIlePheProGlnIle 260  
 DB 934 AAATCTTCTTCTGAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 994  
 QY 261 LeuLeuMetLeuProGlnIleGlnIleGlnIleGlnIleGlnIleGlnIleGlnIleGln 280  
 DB 994 CTCTCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1054  
 QY 281 LeuGlnGlnProLeuValIleLysGlnGlnProGlnGlnGlnGlnGlnGlnGlnGlnGln 300  
 DB 1054 CTTCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1114  
 XX RESULT 2  
 AAA59328  
 ID AAA59328 standard; cDNA: 1367 bp.  
 XX  
 AC AAA59328;  
 XX  
 DT 07-NOV 2000 (first entry)  
 XX  
 DE cDNA encoding an oocyte maturation and proliferation protein Is27.  
 XX  
 KW Oocyte maturation; cell division; cell proliferation; cancer;  
 KW cell differentiation; cell differentiation promoter; fertility treatment;  
 KW cell cycle progression; ss.  
 XX  
 GS Xenopus sp.  
 XX  
 FH Key location/Qualifiers  
 FT CDS 163..1059  
 FT /\*tag a  
 FT /product "Is27"  
 XX  
 PN EP1026244-A1.  
 XX  
 XX 09-AUG-2000.  
 XX  
 XX 03-FEB-1999; 99EP-0102172.  
 XX  
 XX 03-FEB-1999; 99EP-0102172.  
 XX  
 XX (EMBL) EMBL EURO LAB MOLEKULARBIOLOGIE.  
 XX  
 XX WPI: 2000-516092/47.  
 XX  
 XX P-PSDB; AAB07752.  
 XX  
 XX Polynucleotide encoding a protein for inducing oocyte maturation and/or  
 PT promoting cell division, proliferation and differentiation useful for  
 PT treating cancer and disorders associated with fertility.  
 XX  
 XX Claim 1; Page 7; 17pp; English.













QY 108 TyrThrSerGluTyrThrMetAspPheValAlaIleuTyrIleuAlaAspMet 127  
 DB 300 CCGCCGCGCAATACCAACGATTCATCTCTGGCTCTTACCTGGCAATGACACAG 331  
 QY 128 GluGluAspGluGluAspTyrTyrGluIlePheProTrpAlaIleuGlyAspSer 146  
 DB 330 GAGGAG 271  
 QY 147 -----TrpArgGluLeuLeuPheProGlu 153  
 DB 270 TCTGGCAATACCTCTGGCTCTTACCAACGCGGCGGACAGTATPAGGCTGTTAAACCGGAGG 211  
 QY 154 -----PheLeuArgLeuArgAspPheTrpAla 163  
 DB 210 GTCAGCAAGAACCGCTCTCATATAGCCCTCTTCCACAGAACTTGGTTCACAGCTCTCTCT 151  
 QY 164 LysMetAsnTyrArgAlaValValSerArgArgCysCysAspIle 178  
 DB 150 TCCATGAGAGGACAGAGGCTTGGCTTTTGGCGGAGAGAGAGAGAGAGAGAG 106  
 RESULT 9  
 AAS78571  
 ID AAS78571 standard; cDNA: 1405 BP.  
 AC AAS78571;  
 XX  
 XX 13 FEB-2002 (first entry)  
 XX  
 XX DNA encoding novel human diagnostic protein #1475.  
 XX  
 XX Human: chromosome mapping: gene mapping; gene therapy; forensic;  
 KW food supplement; medical imaging; diagnostic; gene therapy; forensic;  
 XX  
 XX Homo sapiens.  
 XX  
 XX W:200175067-A2.  
 XX  
 XX 11-OCT-2001.  
 XX  
 XX 30-MAR-2001; 2001W0-0508641.  
 XX  
 XX 31-MAR-2000; 2000F5 9540217.  
 XX 24 AUG-2000; 2000F5-0649167.  
 XX  
 XX (HYSEQ) HYSEQ INC.  
 XX  
 XX Brimmac RT, Liu C, Tanq YF;  
 XX  
 XX WPI: 2001-649462/73.  
 XX P-PSUB: ABG14384.  
 XX  
 XX Now isolated polynucleotide and encoded polypeptide, useful in  
 PT diagnostics, forensics, gene mapping, identification of mutations  
 PT responsible for genetic disorders or other traits and to assess  
 PT biodiversity.  
 XX  
 XX Claim 1: SEQ ID No 1475; 103pp; English.  
 XX  
 XX the invention relates to isolated polynucleotide (I) and  
 CC polypeptide (II) sequences, (I) is useful as hybridisation probes,  
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome  
 CC and gene mapping, and in recombinant production of (II). The  
 CC polynucleotides are also used in diagnostics as expressed sequence tags  
 CC for identifying expressed genes. (I) is useful in gene therapy techniques  
 CC to restore normal activity of (II) or to treat disease states involving  
 CC (II). (II) is useful for generating antibodies against it, detecting or  
 CC quantifying a polypeptide in tissue, as molecular weight markers and as  
 CC a food supplement. (II) and its binding partners are useful in medical  
 CC imaging of sites expressing (II). (I) and (II) are useful for treating  
 CC disorders involving aberrant protein expression or biological activity.  
 CC the polypeptide and polynucleotide sequences have applications in  
 CC diagnostics, forensics, gene mapping, identification of mutations  
 CC responsible for genetic disorders or other traits to assess biodiversity

CC and to produce other types of data and products dependent on DNA and  
 CC amino acid sequences. AAS78571 AAS78571 represent novel human  
 CC diagnostic coding sequences of the invention.  
 CC Note: The sequence data for this patent did not appear in the printed  
 CC specification, but was obtained in electronic format directly from WPI  
 CC at [http://wipo.int/pub/published\\_pat\\_sequences](http://wipo.int/pub/published_pat_sequences).  
 XX

SQ Sequence 1405 BP; 301 A; 351 C; 306 G; 257 T; 0 other.

Alignment Scores:  
 Pred. No.: 1,416 19 Length: 1405  
 Score: 271.00 Matches: 71  
 Percent Similarity: 54.86% Conserved: 25  
 Best Local Similarity: 40.57% Mismatches: 43  
 Query Match: 16.61% Indels: 42  
 DB: 23 Gaps: 4  
 US-09 889 592-2 (1 400) x AAS78571 (1 1405)  
 QY 35 ArgLysAlaIleuIleProGluArgGluGluGlu SerVal 47  
 DB 679 CCGAAGGCT 708  
 QY 48 LysProLysMetValArgAsnThrHisLeuAsnLeuIleProGluArgGluGluGlu 77  
 DB 739 AAGATGAAAGCTGAAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 708  
 QY 68 TyrArgLeuLeuLeuAsnGluIleIleGluIleProGluLeuMetAspSerCysLeuArg 87  
 DB 799 AAGAGGCT 858  
 QY 88 IleSerArgLysTyrLeuIleAlaMetValLeuAlaTyrPheLeuArgAlaIleuLeu 107  
 DB 859 GTGCGGCAAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 915  
 QY 108 TyrThrSerGluTyrThrMetAsnPheValAlaIleuTyrIleuAlaAspMet 127  
 DB 916 CCGCT 975  
 QY 128 GluGluAspGluGluAspTyrTyrGluIlePheProTrpAlaIleuGlyAspSer 146  
 DB 976 GAGGAG 1035  
 QY 147 -----TrpArgGluLeuLeuPheProGlu 153  
 DB 1046 TCTGGCAATACCTCTGGCTCTTACCAACGCGGCGGACAGTATPAGGCTGTTAAACCGGAGG 1099  
 QY 154 -----PheLeuArgLeuArgAspPheTrpAla 163  
 DB 1096 GCGAGGAG 1155  
 QY 164 LysMetAsnTyrArgAlaValValSerArgArgCysCysAspIle 178  
 DB 1156 TCCATGAGAGGACAGAGGCTTGGCTTTTGGCGGAGAGAGAGAGAGAGAGAG 1200  
 RESULT 10  
 AAS1062  
 ID AAS1062 standard; cDNA: 1405 BP.  
 XX  
 XX AAS1062;  
 XX  
 XX 13 FEB-2002 (first entry)  
 XX  
 XX DNA encoding novel human diagnostic protein #1062.  
 XX  
 XX Human: chromosome mapping; gene mapping; gene therapy; forensic;  
 KW food supplement; medical imaging; diagnostic; gene therapy; forensic;  
 XX  
 XX Homo sapiens.  
 XX  
 XX W:200175067-A2.  
 XX  
 XX 11-OCT-2001.

XX 40 MAR 2001: 2001WO-05086 Q1.  
XX 41 MAR 2001: 2000US-05402 7.  
XX 23 AUG-2000: 2000US-06491 7.  
XX (HYSE-) HYSEQ INC.  
XX Human RT, Liu C, Tang YT;  
XX WPI: 2001-639362/73.  
XX P-PSDB: ABC16879.  
XX  
XX New isolated polynucleotide and encoded polypeptides, useful in  
XX diagnostics, forensic, gene mapping, identification of mutations  
XX responsible for genetic disorders or other traits and to assess  
XX biodiversity.  
XX  
XX Claim 1: SEQ ID No 16870; 103pp: English.  
XX  
XX The invention relates to isolated polynucleotide (I) and  
XX polypeptide (II) sequences. (I) is useful as hybridisation probes,  
XX polymerase chain reaction (PCR) primers, oligomers, and for chromosome  
XX and gene mapping, and in recombinant production of (II). The  
XX polynucleotides are also used in diagnostics as expressed sequence tags  
XX for identifying expressed genes. (I) is useful in gene therapy techniques  
XX to restore normal activity of (II) or to treat disease states involving  
XX (II). (II) is useful for generating antibodies against it, detecting or  
XX quantitating a polypeptide in tissue, as molecular weight markers and as  
XX a food supplement. (II) and its binding partners are useful in medical  
XX imaging of sites expressing (II). (I) and (II) are useful for treating  
XX disorders involving aberrant protein expression or biological activity.  
XX The polypeptide and polynucleotide sequences have applications in  
XX diagnostics, forensic, gene mapping, identification of mutations  
XX responsible for genetic disorders or other traits to assess biodiversity  
XX and to produce other types of data and products dependent on DNA and  
XX amino acid sequences. AAS64167-AAS64564 represent novel human  
XX diagnostic coding sequences of the invention.  
XX Note: the sequence data for this patent did not appear in the printed  
XX specification, but was obtained directly from the format directly from WIPO  
XX at ftp://wipo.int/pub/pubseq/16870-16879-16880-16881-16882-16883-16884-16885-16886-16887-16888-16889-16890-16891-16892-16893-16894-16895-16896-16897-16898-16899-16900-16901-16902-16903-16904-16905-16906-16907-16908-16909-16910-16911-16912-16913-16914-16915-16916-16917-16918-16919-16920-16921-16922-16923-16924-16925-16926-16927-16928-16929-16930-16931-16932-16933-16934-16935-16936-16937-16938-16939-16940-16941-16942-16943-16944-16945-16946-16947-16948-16949-16950-16951-16952-16953-16954-16955-16956-16957-16958-16959-16960-16961-16962-16963-16964-16965-16966-16967-16968-16969-16970-16971-16972-16973-16974-16975-16976-16977-16978-16979-16980-16981-16982-16983-16984-16985-16986-16987-16988-16989-16990-16991-16992-16993-16994-16995-16996-16997-16998-16999-17000-17001-17002-17003-17004-17005-17006-17007-17008-17009-17010-17011-17012-17013-17014-17015-17016-17017-17018-17019-17020-17021-17022-17023-17024-17025-17026-17027-17028-17029-17030-17031-17032-17033-17034-17035-17036-17037-17038-17039-17040-17041-17042-17043-17044-17045-17046-17047-17048-17049-17050-17051-17052-17053-17054-17055-17056-17057-17058-17059-17060-17061-17062-17063-17064-17065-17066-17067-17068-17069-17070-17071-17072-17073-17074-17075-17076-17077-17078-17079-17080-17081-17082-17083-17084-17085-17086-17087-17088-17089-17090-17091-17092-17093-17094-17095-17096-17097-17098-17099-17100-17101-17102-17103-17104-17105-17106-17107-17108-17109-17110-17111-17112-17113-17114-17115-17116-17117-17118-17119-17120-17121-17122-17123-17124-17125-17126-17127-17128-17129-17130-17131-17132-17133-17134-17135-17136-17137-17138-17139-17140-17141-17142-17143-17144-17145-17146-17147-17148-17149-17150-17151-17152-17153-17154-17155-17156-17157-17158-17159-17160-17161-17162-17163-17164-17165-17166-17167-17168-17169-17170-17171-17172-17173-17174-17175-17176-17177-17178-17179-17180-17181-17182-17183-17184-17185-17186-17187-17188-17189-17190-17191-17192-17193-17194-17195-17196-17197-17198-17199-17200-17201-17202-17203-17204-17205-17206-17207-17208-17209-17210-17211-17212-17213-17214-17215-17216-17217-17218-17219-17220-17221-17222-17223-17224-17225-17226-17227-17228-17229-17230-17231-17232-17233-17234-17235-17236-17237-17238-17239-17240-17241-17242-17243-17244-17245-17246-17247-17248-17249-17250-17251-17252-17253-17254-17255-17256-17257-17258-17259-17260-17261-17262-17263-17264-17265-17266-17267-17268-17269-17270-17271-17272-17273-17274-17275-17276-17277-17278-17279-17280-17281-17282-17283-17284-17285-17286-17287-17288-17289-17290-17291-17292-17293-17294-17295-17296-17297-17298-17299-17300-17301-17302-17303-17304-17305-17306-17307-17308-17309-17310-17311-17312-17313-17314-17315-17316-17317-17318-17319-17320-17321-17322-17323-17324-17325-17326-17327-17328-17329-17330-17331-17332-17333-17334-17335-17336-17337-17338-17339-17340-17341-17342-17343-17344-17345-17346-17347-17348-17349-17350-17351-17352-17353-17354-17355-17356-17357-17358-17359-17360-17361-17362-17363-17364-17365-17366-17367-17368-17369-17370-17371-17372-17373-17374-17375-17376-17377-17378-17379-17380-17381-17382-17383-17384-17385-17386-17387-17388-17389-17390-17391-17392-17393-17394-17395-17396-17397-17398-17399-17400-17401-17402-17403-17404-17405-17406-17407-17408-17409-17410-17411-17412-17413-17414-17415-17416-17417-17418-17419-17420-17421-17422-17423-17424-17425-17426-17427-17428-17429-17430-17431-17432-17433-17434-17435-17436-17437-17438-17439-17440-17441-17442-17443-17444-17445-17446-17447-17448-17449-17450-17451-17452-17453-17454-17455-17456-17457-17458-17459-17460-17461-17462-17463-17464-17465-17466-17467-17468-17469-17470-17471-17472-17473-17474-17475-17476-17477-17478-17479-17480-17481-17482-17483-17484-17485-17486-17487-17488-17489-17490-17491-17492-17493-17494-17495-17496-17497-17498-17499-17500-17501-17502-17503-17504-17505-17506-17507-17508-17509-17510-17511-17512-17513-17514-17515-17516-17517-17518-17519-17520-17521-17522-17523-17524-17525-17526-17527-17528-17529-17530-17531-17532-17533-17534-17535-17536-17537-17538-17539-17540-17541-17542-17543-17544-17545-17546-17547-17548-17549-17550-17551-17552-17553-17554-17555-17556-17557-17558-17559-17560-17561-17562-17563-17564-17565-17566-17567-17568-17569-17570-17571-17572-17573-17574-17575-17576-17577-17578-17579-17580-17581-17582-17583-17584-17585-17586-17587-17588-17589-17590-17591-17592-17593-17594-17595-17596-17597-17598-17599-17600-17601-17602-17603-17604-17605-17606-17607-17608-17609-17610-17611-17612-17613-17614-17615-17616-17617-17618-17619-17620-17621-17622-17623-17624-17625-17626-17627-17628-17629-17630-17631-17632-17633-17634-17635-17636-17637-17638-17639-17640-17641-17642-17643-17644-17645-17646-17647-17648-17649-17650-17651-17652-17653-17654-17655-17656-17657-17658-17659-17660-17661-17662-17663-17664-17665-17666-17667-17668-17669-17670-17671-17672-17673-17674-17675-17676-17677-17678-17679-17680-17681-17682-17683-17684-17685-17686-17687-17688-17689-17690-17691-17692-17693-17694-17695-17696-17697-17698-17699-17700-17701-17702-17703-17704-17705-17706-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## Alignment Scores:

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Prod. No.: 396 47 575
Score: 1042.00 Matches: 400
Percent Similarity: 100.00% Conserved: 4
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 (100%)

US-09-889-592-2 (1-300) x AX034536 (1-107)

QY 1 MetArgHisMetGlnSerValThrArgAlaSerSerHisCysGlySerValValysGln 20
DB 214 AIGAGGCAATGCCAGGCTAATCCCGGCGCCACCCACCTTGTGGCAGCG35GTGACGAC 273
QY 21 ValIleGlyLysGlyHisProHisAlaArgValValGlyLysAlaGlnIlePro 40
DB 274 GTTATGGGAGAGGGAATGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 333
QY 41 GlnArgGluGluSerValLysProLysMetValArgAsnThrHisLeuAsnGln 60
DB 434 GACACAGAGAGGCTTGTCTACTAAACCTTAAATAGATGGGNAATATGCAATTTACAG 393
QY 61 ProGlnGluArgGlnAlaPheGlyArgGlnLeuGlnIleLeuGlnLeu 80
DB 494 GATAGGACCGGACGACGCTGTACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 453
QY 81 SerMetAspSerCysLeuArgIleSerAspLysTyrLeuIleAlaMetValLeuAlaTyr 100
DB 454 TCTATGGAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 513
QY 141 PhdysArgAlaAlaAlaGlyLeuTyrHisSerValThrHisMetAspHisPheValIle 120
DB 514 TTAAAGCGGAGAGAGAGAGCTTAAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 573
QY 161 LeuLeuAlaAspHisMetGlnSerValThrArgAlaArgValValLeuLeuPhePro 140
DB 574 CAGCACTCTGGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 633
QY 181 TrpAlaLeuGlyAspSerTrpArgValLeuPheGlnPheLeuArgLeuArgAspAsp 160
DB 634 TGAGAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 693
QY 201 PhdysAlaLysMetAspHisArgAlaValAlaSerArgArgValCysAspGluValMet 180
DB 694 TTCTAGGCTAATAATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 753
QY 221 SerLysAspProThrHisTrpAlaValPheArgAspProMetHisHisSerGlyVal 200
DB 754 TCTAAGAGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 813
QY 241 MetArgGlyTrpLeuArgAlaGlnLeuPheHisLeuAlaPheGlySerTrpLeuPro 220
DB 814 ATCTAGGCTAATAATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 873
QY 261 AsnArgGlyHisLeuGlySerHisArgValValValValValValValValValVal 240
DB 874 GATAGAGTGTACACTTTGGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 933
QY 281 AsnSerSerSerTrpGlnArgValPheHisThrArgAspGlnTrpSerGlnGln 260
DB 934 AATGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 993
QY 301 LeuLeuMetLeuProGlnIleLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 280
DB 994 CTTCATCATGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1053
QY 321 GlnGlnGluProGlnValGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 300
DB 1054 CTCTAAGAGAGGATGGTTGATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1113
RESULT 1
XIA249978 LOCUS

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## DEFINITION

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Xenopus laevis mRNA for p33 ringo (1s26 gene), clone 5.
VERSION
AJ249978 1 GI:6066823
FEATURES
1s26 gene, p33 ringo.
SOURCE
Xenopus laevis.
ORGANISM
Xenopus laevis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
Xenopodidae; Xenopus.
REFERENCE
1 (bases 1 to 1376)
Perly, L., Blazquez, M., Palmer, A., Eritja, R. and Nebreda, A.R.
A novel p34(ccd2)-binding and activating protein that is necessary
and sufficient to trigger G(2)/M progression in Xenopus oocytes
Genes Dev. 13 (16): 2177-2189 (1999)
GENES
99396721
10465793
2 (bases 1 to 1376)
NEBREDA, A.R.
DIRECT SUBMISSION
SUBMITTED (12-OCT-1999) NEBREDA, A.R., DEVELOPMENTAL BIOLOGY
PROGRAMME, EMBL, MEYERHOFSTRASSE 1, 69117 HEIDELBERG, GERMANY
FEATURES
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/db_xref="taxon:8355"
214..1113
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214..1113
/ gene="1s26/clone 5"
/function="triggers oocyte meiotic maturation"
/codon_start=1
/product="p33 ringo"
/protein_id="CA58366.1"
/db_xref="GI:6066824"
/translation="MHIMQSVIRATSLNAGVIVIKRHPHAPVVGAPKAQIPERE
LSVKPKVNRNTHNLQDPOCALYRLLENKQIOEFLSDSCURISPKYLIAVLAYFK
RACLYTSEYITMRFVVALYLANDMEDEEDYKVEIFPWALGDSWRKELHQQFRLKDDF
WAKNRYAVSVRCCDVMKSDPTHWALDRPHHSGAMRGTRLRNEDFSPRGCLT
PASCTLCRKAGVCDGSGVSHNSSPSEQUEIFHYINREWSQELLMSPDLLDPECTHD
LHIQLEPLVLEPDTALEWHHL"
BASE COUNT 358 a 331 c 336 g 351 t
TAGIN

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## Alignment Scores:

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Prod. No.: 3,776,144 Length: 1376
Score: 1594.50 Matches: 295
Percent Similarity: 99.90% Conserved: 2
Best Local Similarity: 98.33% Mismatches: 2
Query Match: 97.70% Indels: 1
DB: 5 Gaps: 1

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US-09-889-592-2 (1-300) x XIA249978 (1-1376)

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QY 1 MetArgHisMetGlnSerValThrArgAlaSerSerHisCysGlySerValValysGln 20
DB 214 AIGAGGCAATGCCAGGCTAATCCCGGCGCCACCCACCTTGTGGCAGCG35GTGACGAC 273
QY 21 ValIleGlyLysGlyHisProHisAlaArgValValGlyLysAlaGlnIlePro 40
DB 274 GTTATGGGAGAGGGAATGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 333
QY 41 GlnArgGluGluSerValLysProLysMetValArgAsnThrHisLeuAsnGln 60
DB 434 GACACAGAGAGGCTTGTCTACTAAACCTTAAATAGATGGGNAATATGCAATTTACAG 393
QY 61 ProGlnGluArgGlnAlaPheGlyArgGlnLeuGlnIleLeuGlnLeu 80
DB 494 GATAGGACCGGACGACGCTGTACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 453
QY 81 SerMetAspSerCysLeuArgIleSerAspLysTyrLeuIleAlaMetValLeuAlaTyr 100
DB 454 TCTATGGAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 513

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XIA249978 LOCUS





[illegible]

RESULT 7	
AF492485	
Locus	1896 bp mRNA linear Feb 07 AUG 2002
DEFINITION	Rattus norvegicus cIS4 mRNA, complete cds.
ACCESSION	AF492485
KEYWORDS	AF492485.1 GI:20967260 Rattus norvegicus. Rattus norvegicus Eukaryotic; Metazoan; Chordata; Vertebrate; Euteleostomi; Mammalia; Eutheria; Rodentia; Muridae; Murinae;
SOURCE ORGANISM	Rattus

REFERENCE	1	{bases 1 to 1896}
AUTHOR	Zhao,L. and Jia,M.	
TITLE	Gene related to spermatogenesis	
JOURNAL	Unpublished	
REFERENCE	2	{bases 1 to 1896}
AUTHOR	Zhao,L. and Jia,M.	
TITLE	Direct Submission	
JOURNAL	Submitted (13 MAR 2002) Reproductive Endocrinology, National Institution of Family Planning, No.12,JiefangSt., Haidianqu, Beijing 100081, China P.R.	
FEATURES	Location/Qualifiers	
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	/translation:"MHNNWSTTTPVIVHVSSENFQGLFEELVEKPEFLEWQ ASPKNHNKKPRPGPCLIQROEMAFKEFLIDDLIQDEIMWCCKIAKYLLAM IEVYEPKELISELQINELALVLANTVEEFPAKYEIFRWALGWKPPLFNPL KLQDQLWDITRAVSHRCCEVMALASHITWHPERSVMSHGKAARTNRQEVILFR KRSATQVETLVVPSPPSSSSSSSSSVLTLPSPSSSLINSLSMDMIGDPSSQ ANYSVCANHQSNNKLNENFKTKSMGEAFSE"	
BASE COUNT	646 a 359 c 385 g 506 t	
ORIGIN		
Alignment Scores:		
Pred. No.:	9,41e-49	Length: 1896
Score:	609.00	Matches: 129
Percent Similarity:	62.61%	Conservative: 44
Best Local Similarity:	46.24%	Mismatches: 94
Query Match:	37.14%	Indels: 12
DB:	10	Gaps: 6
US-09-889 592 2 (1 400) x AF492485 (1 1896)		
QY	1	MetArchiSmctGlnSerValIprArqAlasrScfIecysSlcSrCllyValylsGln 20 
Dd	88	ATGGGCATAATCAGATGTCTTGACACACACTACTCTACTTTATGTAATAA 147 
QY	21	ValllcltPlstLYlStPrHisAlaaValvAlcYlaAlaGlssAla 47 
Dd	148	GGTCAAAATGGTCACATCAAAACAGAACCGCTAGCTCAAGAGTCTTATAA 297 
QY	48	- - - - - GlnIleProGluAlaGlnGlnSerValylsPrdylsMetValAlaAsn 54

Alignment Scores:			
pred. No.:	9,418,49	Length:	1806
Score:	609.00	Matches:	129
Percent Similarity:	62.61%	Conserved Sites:	94
Best Local Similarity:	46.24%	Mismatched Sites:	55
Query Match:	37.14%	Indels:	12
LB:	10	Gaps:	6
US-09-889,592 (1,400)	X	AF492485 (1,896)	

[illegible]







## COMMENT

\* If this is a continuing accession, currently  
\* consists of a continuing series of the plates  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the units are represented as  
\* gaps of N, but the exact sizes of the gaps are unknown.  
\* This record will be related with the finished sequence,  
\* as soon as it is available and the accession number will  
\* be preserved.

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160	81526	TGAGCTTGAGCTCTCTGGTAAGAAATTTGAAAATATATGAAAGAGATGAAAGG	81685
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200	81786	CCCAAAATCTGASATTTTTCGATGGGCGCTGGGAAAAACATTCGTGTGTTCAGGAC	81745
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240	81746	TCCTTGAAATAGAGAGAAATAAATTTGAGGAAATGATATGATATTTGAGAGTATTTG	81805
260	174	ArgCysCysAspGlu	178









1000 JOURNAL OF CLIMATE



